We claim:

1. A method of diagnosing or determining if a patient has cancer or is at increased risk of cancer, the method comprising testing a FANC gene for the presence of a cancer-associated coding change, wherein said presence of one or more cancer-associated coding changes is indicative of cancer or an increased risk of cancer in said patient.

2. The method according to claim 1, wherein said cancer is pancreatic cancer.

3. The method according to claim 1, wherein said cancer-associated coding change in the FANCC gene is selected from the group consisting of : mutations of the FANCA gene listed in Table 2, mutations of the FANCC gene listed in Table 3, mutations of the FANCD2 gene listed in Table 4, mutations of the FANCE gene listed in Table 5, mutations of the FANCF gene listed in Table 6, mutations of the FANCG gene listed in Table 7.

4. A method of determining if a patient has cancer, or is at increased risk of developing cancer comprising the steps of: (a) providing a DNA sample from said patient; (b) amplifying the FANC gene from said patient with the FANC gene-specific polynucleotide primers; (c) sequencing the amplified FANCC gene; and (d) comparing the FANC gene sequence from said patient to a reference FANC gene sequence, where a discrepancy between the two gene sequences indicates the presence of a cancer-associated coding change; wherein the presence of one or more cancer-associated coding changes indicates said patient has cancer or is at an increased risk of developing cancer.

5. The method according to claim 4, wherein said cancer-associated coding change in the FANCC gene is selected from the group consisting of : mutations of the FANCA gene listed in Table 2, mutations of the FANCC gene listed in Table 3, mutations of the FANCD2 gene listed in Table 4, mutations of the FANCE gene listed in Table 5, mutations of the FANCF gene listed in Table 6, mutations of the FANCG gene listed in Table 7.

6. The methods according to either of claims 4 and 5, wherein said cancer is pancreatic cancer.

7. A method of treating a patient having cancer or having a risk of developing cancer who has one or more cancer-associated coding changes in the FANC genes comprising the step of administering a therapeutically effective amount of a chemotherapeutic DNA cross-linking agent.

8. The method according to claim 7, wherein said cancer-associated coding change in the FANCC gene is selected from the group consisting of : mutations of the FANCA gene listed in Table 2, mutations of the FANCC gene listed in Table 3, mutations of the FANCD2 gene listed in Table 4, mutations of the FANCE gene listed in Table 5, mutations of the FANCF gene listed in Table 6, mutations of the FANCG gene listed in Table 7.

9. The methods according to either of claims 7 and 8, wherein the said cancer is pancreatic cancer.

10. The methods according to either of claims 7 and 8, wherein the therapeutically effective amount of a chemotherapeutic DNA cross-linking agent is a low dose of agent.

11. The method according to claim 10, wherein the low dose of agent is a daily dose at one-twentieth to one-fifteenth the standard dose.

12. The method according to any of claims 7-11, wherein said chemotherapeutic cross-linking agent is mitomycin C.

13. The method according to any of claims 7-11, wherein said chemotherapeutic cross-linking agent is cisplatin.

14. A method for screening for a cancer therapeutic, the method comprising the steps of: (a) providing one or more cells containing one or more cancer associated coding changes in the FANC genes; (b) growing said cells in the presence of a potential

cancer therapeutic; and (c) determining the rate of growth of said cells in the presence of said potential cancer therapeutic relative to the rate of growth of equivalent cells grown in the absence of said potential cancer therapeutic; wherein a reduced rate of growth of said cells in the presence of said potential cancer therapeutic, relative to the rate of growth of equivalent cells grown in the absence of said potential cancer therapeutic, indicates that the potential cancer then is a cancer therapeutic.

15. The method of claim 21, wherein said cells containing one or more cancer associated coding changes in the FANC genes are distributed in a array.

16. A kit for detecting cancer-associated coding changes in the FANC gene, comprising a polynucleotide primer pair specific for the FANC gene, a reference FANC gene sequence and packaging materials therefore.

17. A microarray containing one or more nucleic acid sequences from one or more FANC genes with cancer-associated coding changes.

18. The microarray of claim 27, wherein said cancer-associated coding change in the FANCC gene is selected from the group consisting of : mutations of the FANCA gene listed in Table 2, mutations of the FANCC gene listed in Table 3, mutations of the FANCD2 gene listed in Table 4, mutations of the FANCE gene listed in Table 5, mutations of the FANCF gene listed in Table 6, mutations of the FANCG gene listed in Table 7.

19. The microarray of claim 18, wherein said cancer-associated coding change in the FANCG gene is selected from the group consisting of : E105ter with loss of heterozygosity; and S7F with loss of heterozygosity.

30. The microarray of claim 27, wherein said cancer-associated coding change in the BRCA2 gene is 6174delT with loss of hetreozygosity.

31. A method of determining if a patient has cancer, or is at increased risk of developing cancer, said method comprising the steps of: (a) providing the microarray of claim 27; (b) providing a nucleic acid sample from said patient; (c) hybridizing said

nucleic acid sample to said nucleic acid sequences from FANCC, FANCG or BRCA2 genes with cancer-associated coding changes on said microarray; and (d) detecting the presence of cancer-associated coding changes in the nucleic acid sample from said patient; wherein said detecting the presence of cancer-associated coding changes is indicative of a patient who has cancer, or is at increased risk of developing cancer.